


Exhibit II

Query: SEQ ID NO: 8

BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)**Nucleotide Sequence (19 letters)**Results for: lcl|9600 None(19bp) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|9600

Description

None

Molecule type

nucleic acid

Query Length

19

Database Name

nr

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ [Citation](#)Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Distance tree of results](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Database

Posted date	Dec 28, 2008 5:47 PM
Number of letters	252,991,180
Number of sequences	7,851,115
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Length adjustment	17
Effective length of query	2
Effective length of database	25589522225
Effective search space	51179044450
Effective search space used	51179044450

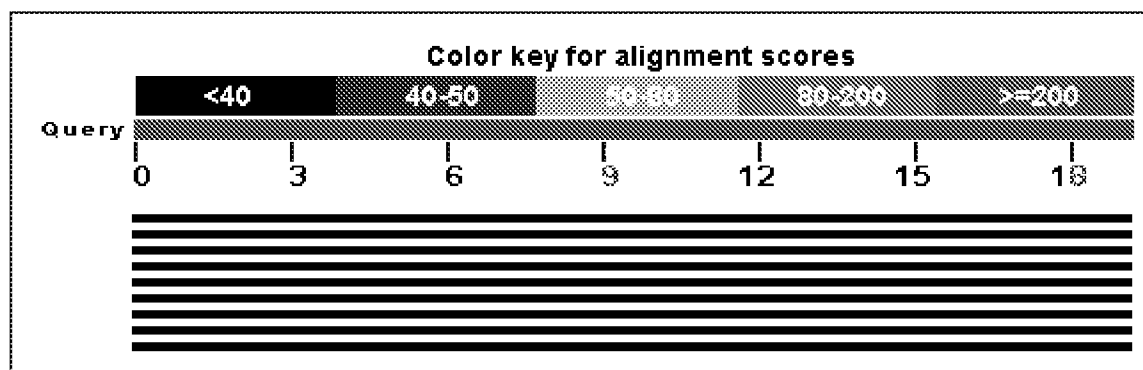
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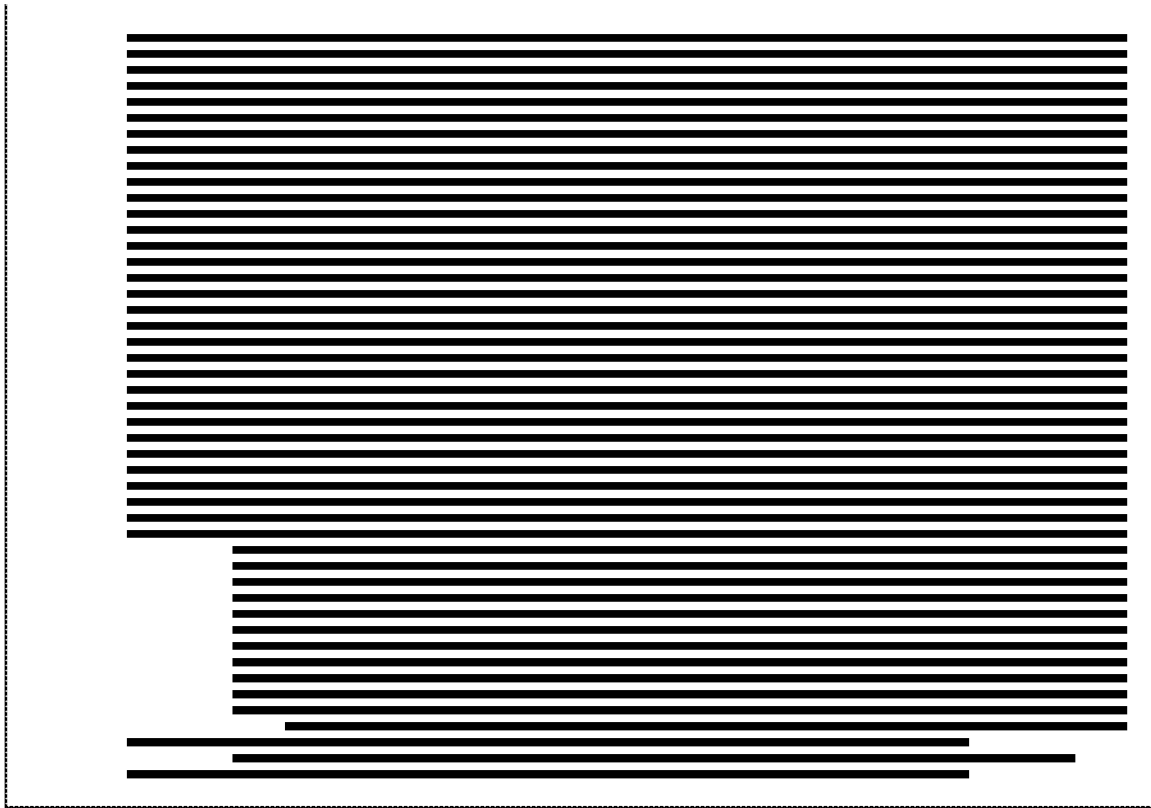
Graphic Summary

Distribution of 112 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Descriptions](#)

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer


Sequences producing significant alignments:

(Click headers to sort columns)

XM_001916096.1	PREDICTED: Equus caballus similar to glutathione peroxidase 1 (LOC100053396), mRNA	38.2	38.2	100%	0.17	100%	
NM_001115119.1	Canis lupus familiaris glutathione peroxidase 1 (GPX1), mRNA	38.2	38.2	100%	0.17	100%	  
XR_038530.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	38.2	38.2	100%	0.17	100%	
XR_038228.1	PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA	38.2	38.2	100%	0.17	100%	
NM_001077512.2	Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA	38.2	38.2	100%	0.17	100%	
AK239914.1	Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus	38.2	38.2	100%	0.17	100%	
AK231261.1	Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine	38.2	38.2	100%	0.17	100%	
AB121000.1	Callithrix jacchus gpx1 mRNA for glutathione peroxidase 1, complete cds	38.2	38.2	100%	0.17	100%	
AB120996.1	Pan troglodytes gpx1 mRNA for glutathione peroxidase 1, complete cds	38.2	38.2	100%	0.17	100%	
AK225835.1	Homo sapiens mRNA for Glutathione peroxidase 1 variant, clone: FCC127C01	38.2	38.2	100%	0.17	100%	 
XR_013650.1	PREDICTED: Macaca mulatta similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) (LOC706732), mRNA	38.2	38.2	100%	0.17	100%	 
AY966403.1	Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA, complete cds	38.2	38.2	100%	0.17	100%	
AY743601.1	Sus scrofa cytosolic glutathione peroxidase mRNA, partial cds	38.2	38.2	100%	0.17	100%	 
BC007865.2	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:14399 IMAGE:4301275), complete cds	38.2	38.2	100%	0.17	100%	 
BC000742.2	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:2335 IMAGE:3505654), complete cds	38.2	38.2	100%	0.17	100%	 
BC070258.1	Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:88245 IMAGE:6452792), complete cds	38.2	38.2	100%	0.17	100%	 
AY572225.1	Canis familiaris glutathione peroxidase 1 mRNA, partial cds	38.2	38.2	100%	0.17	100%	 
AC135371.2	Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence	38.2	38.2	100%	0.17	100%	
AY327818.1	Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cds	38.2	38.2	100%	0.17	100%	
NM_214201.1	Sus scrofa glutathione peroxidase 1	38.2	38.2	100%	0.17	100%	 

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[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>ref|XM_001916096.1|  PREDICTED: Equus caballus similar to glutathione peroxidase 1 (LOC100053396), mRNA
Length=606

GENE ID: 100053396 LOC100053396 | similar to glutathione peroxidase 1 [Equus caballus]

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 322    TGAAGTTGGGCTCGAACCC 304
```

>ref|NM_001115119.1|  Canis lupus familiaris glutathione peroxidase 1 (GPX1)
Length=838

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 343    TGAAGTTGGGCTCGAACCC 325
```

>ref|XR_038530.1|  PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA
Length=876

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 361    TGAAGTTGGGCTCGAACCC 343
```


>ref|XR_038228.1|  PREDICTED: Homo sapiens misc_RNA (LOC441481), miscRNA
Length=878

GENE ID: 441481 LOC441481 | similar to Glutathione peroxidase 1 (GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) [Homo sapiens]

Score = 38.2 bits (19), Expect = 0.17

Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 363    TGAAGTTGGGCTCGAACCC 345
```

>ref|NM_001077512.2|  Pan troglodytes glutathione peroxidase 1 (GPX1), mRNA
Length=613

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]
(10 or fewer PubMed links)


Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 329    TGAAGTTGGGCTCGAACCC 311
```

>dbj|AK239914.1|  Sus scrofa mRNA, clone:UTR010010G07, expressed in uterus
Length=912

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 420    TGAAGTTGGGCTCGAACCC 402
```

>dbj|AK231261.1|  Sus scrofa mRNA, clone:ITT010025D10, expressed in intestine
Length=936


Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 435    TGAAGTTGGGCTCGAACCC 417
```

>dbj|AB121000.1| Callithrix jacchus gpx1 mRNA for glutathione peroxidase 1, comp
cds
Length=606

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
Sbjct 322    TGAAGTTGGGCTCGAACCC 304
```


>dbj|AB120996.1|  Pan troglodytes gpx1 mRNA for glutathione peroxidase 1, compl
cds
Length=606

GENE ID: 461015 GPX1 | glutathione peroxidase 1 [Pan troglodytes]
(10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||
```


Sbjct 322 TGAAGTTGGGCTCGAACCC 304

>dbj|AK225835.1|  Homo sapiens mRNA for Glutathione peroxidase 1 variant, clo
FCC127C01
Length=874

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19
|||||
Sbjct 331 TGAAGTTGGGCTCGAACCC 313

>ref|XR_013650.1|  PREDICTED: Macaca mulatta similar to Glutathione peroxidase
(GSHPx-1) (GPx-1) (Cellular glutathione peroxidase) (LOC706732),
mRNA
Length=811

GENE ID: 706732 LOC706732 | similar to Glutathione peroxidase 1 (GSHPx-1)
(GPx-1) (Cellular glutathione peroxidase) [Macaca mulatta]


Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19
|||||
Sbjct 313 TGAAGTTGGGCTCGAACCC 295

>gb|AY966403.1| Callithrix jacchus cytosolic glutathione peroxidase (Gpx-1) mRNA
complete cds
Length=858

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


Query 1 TGAAGTTGGGCTCGAACCC 19
|||||
Sbjct 345 TGAAGTTGGGCTCGAACCC 327

>gb|AY743601.1|  Sus scrofa cytosolic glutathione peroxidase mRNA, partial cd
Length=256

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]
(10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

Query 1 TGAAGTTGGGCTCGAACCC 19
|||||
Sbjct 95 TGAAGTTGGGCTCGAACCC 77


>gb|BC007865.2|  Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MGC:
IMAGE:4301275), complete cds
Length=851

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)

Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||||
Sbjct 338    TGAAGTTGGGCTCGAACCC 320
```

>gb|BC000742.2|  Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:3505654), complete cds
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||||
Sbjct 351    TGAAGTTGGGCTCGAACCC 333
```

>gb|BC070258.1|  Homo sapiens glutathione peroxidase 1, mRNA (cDNA clone MG IMAGE:6452792), complete cds
Length=866

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||||
Sbjct 344    TGAAGTTGGGCTCGAACCC 326
```

>gb|AY572225.1|  Canis familiaris glutathione peroxidase 1 mRNA, partial cds
Length=434

GENE ID: 442961 GPX1 | glutathione peroxidase 1 [Canis lupus familiaris]


Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||||
Sbjct 283    TGAAGTTGGGCTCGAACCC 265
```

>gb|AC135371.2|  Homo sapiens X BAC RP11-142G7 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length=25901

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Plus



```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||||
Sbjct 8885   TGAAGTTGGGCTCGAACCC 8903
```

>gb|AY327818.1|  Homo sapiens glutathione peroxidase 1 (GPX1) gene, complete cd
Length=4877

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 2772   TGAAGTTGGGCTCGAACCC 2754
```

>ref|NM_214201.1|  Sus scrofa glutathione peroxidase 1 (GPX1), mRNA
 gb|AF532927.1|  Sus scrofa cytosolic glutathione peroxidase (GPX1) mRNA, com
 cds
 Length=803

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]
 (10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 343     TGAAGTTGGGCTCGAACCC 325
```

>dbj|AB120999.1| Cebus apella gpx1 mRNA for glutathione peroxidase 1, complete
 cds
 Length=606

Score = 38.2 bits (19), Expect = 0.17
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 322     TGAAGTTGGGCTCGAACCC 304
```

>dbj|AB120998.1| Hylobates lar gpx1 mRNA for glutathione peroxidase 1, complete
 cds
 Length=606


Score = 38.2 bits (19), Expect = 0.17
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 322     TGAAGTTGGGCTCGAACCC 304
```

>dbj|AB120997.1| Pongo pygmaeus gpx1 mRNA for glutathione peroxidase 1, complete
 cds
 Length=606

Score = 38.2 bits (19), Expect = 0.17
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 322     TGAAGTTGGGCTCGAACCC 304
```


>gb|M83094.1|HUMGLPEX  Homo sapiens cytosolic selenium-dependent glutathione
 gene, complete cds, and rhoh12 gene, 3' end
 Length=4407

Score = 38.2 bits (19), Expect = 0.17
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

```

Query   1      TGAAGTTGGGCTCGAACCC   19
          |||||
Sbjct   3157    TGAAGTTGGGCTCGAACCC   3139

```

>emb|Y00483.1|HSGSHPXG  Human gene for glutathione peroxidase
Length=1733


GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```

Query   1      TGAAGTTGGGCTCGAACCC   19
          |||||
Sbjct   1073    TGAAGTTGGGCTCGAACCC   1055

```

>emb|Y00433.1|HSGSHPX  Human mRNA for glutathione peroxidase (EC 1.11.1.9.)
Length=1134


GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```

Query   1      TGAAGTTGGGCTCGAACCC   19
          |||||
Sbjct   640    TGAAGTTGGGCTCGAACCC   622

```

>emb|X13710.1|HSPEROXP  H.sapiens unspliced mRNA for glutathione peroxidase
Length=1100


GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```

Query   1      TGAAGTTGGGCTCGAACCC   19
          |||||
Sbjct   606    TGAAGTTGGGCTCGAACCC   588

```

>emb|X13709.1|HSPEROXR  Human gpx1 mRNA for glutathione peroxidase
Length=819



GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```

Query   1      TGAAGTTGGGCTCGAACCC   19
          |||||
Sbjct   327    TGAAGTTGGGCTCGAACCC   309


```

>ref|NM_001085444.1|  Oryctolagus cuniculus glutathione peroxidase 1 (GPX1),
emb|X13837.1|OCGPO  Rabbit mRNA for glutathione peroxidase (EC 1.11.1.9)
Length=760

GENE ID: 100009258 GPX1 | glutathione peroxidase 1 [Oryctolagus cuniculus]
(10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 337    TGAAGTTGGGCTCGAACCC 319
```

>gb|M21304.1|HUMGLP  Human glutathione peroxidase (GPX1) mRNA, complete cds
Length=856

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 363    TGAAGTTGGGCTCGAACCC 345
```

>emb|AJ010340.1|SAJ10340  Sus scrofa mRNA for glutathione peroxidase, partial
Length=348

GENE ID: 397403 GPX1 | glutathione peroxidase 1 [Sus scrofa]
(10 or fewer PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 100    TGAAGTTGGGCTCGAACCC 82
```

>emb|CR626479.1|  full-length cDNA clone CS0CAP001YI17 of Thymus of Homo sapi
(human)
Length=838

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 342    TGAAGTTGGGCTCGAACCC 324
```

>emb|CR620255.1|  full-length cDNA clone CS0DD004YA07 of Neuroblastoma Cot 50
of Homo sapiens (human)
Length=828

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
          |||||
Sbjct 351    TGAAGTTGGGCTCGAACCC 333
```

>emb|CR614747.1|  full-length cDNA clone CS0DI086YP09 of Placenta Cot 25-norm of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||
Sbjct 376    TGAAGTTGGGCTCGAACCC 358
```

>emb|CR601795.1|  full-length cDNA clone CS0DI068YJ17 of Placenta Cot 25-norm of Homo sapiens (human)
Length=792

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||
Sbjct 296    TGAAGTTGGGCTCGAACCC 278
```

>emb|CR595371.1|  full-length cDNA clone CS0DC025YE23 of Neuroblastoma Cot 25 of Homo sapiens (human)
Length=849

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||
Sbjct 353    TGAAGTTGGGCTCGAACCC 335
```

>dbj|AK130160.1|  Homo sapiens cDNA FLJ26650 fis, clone MPE04848, highly similar to Glutathione peroxidase (EC 1.11.1.9)
Length=863

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

```
Query 1      TGAAGTTGGGCTCGAACCC 19
           |||
Sbjct 369    TGAAGTTGGGCTCGAACCC 351
```

>gb|AC121247.2|  Homo sapiens chromosome 3 clone RP11-3B7, complete sequence
Length=170787

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


```
Query 1      TGAAGTTGGGCTCGAACCC 19
```

Sbjct 23229 |||||TGAAGTTGGGCTCGAACCC 23211

>dbj|AB105162.1| Macaca fuscata mRNA for cytosolic glutathione peroxidase, complete cds
Length=606

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


Query 1 TGAAGTTGGGCTCGAACCC 19
Sbjct 322 |||||TGAAGTTGGGCTCGAACCC 304

>ref|NM_000581.2|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript 1, mRNA
Length=921

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


Query 1 TGAAGTTGGGCTCGAACCC 19
Sbjct 408 |||||TGAAGTTGGGCTCGAACCC 390

>ref|NM_201397.1|  Homo sapiens glutathione peroxidase 1 (GPX1), transcript 2, mRNA
Length=1200

GENE ID: 2876 GPX1 | glutathione peroxidase 1 [Homo sapiens]
(Over 100 PubMed links)

Score = 38.2 bits (19), Expect = 0.17
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus


Query 1 TGAAGTTGGGCTCGAACCC 19
Sbjct 687 |||||TGAAGTTGGGCTCGAACCC 669

>ref|XM_001788272.1|  PREDICTED: Bos taurus hypothetical protein LOC100139030 mRNA
Length=761

GENE ID: 100139030 LOC100139030 | hypothetical protein LOC100139030 [Bos taurus]

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 3 AAGTTGGGCTCGAACCC 19
Sbjct 504 |||||AAGTTGGGCTCGAACCC 520

>ref|NM_174076.3|  Bos taurus glutathione peroxidase 1 (GPX1), mRNA
Length=926

GENE ID: 281209 GPX1 | glutathione peroxidase 1 [Bos taurus]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)